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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 1871.

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			Description		BG415676 HVSMEk000	BF625060 HVSMEa000		BE345465 946035B01	BI178113 EST519058	BE455437 HVSMEq001	AIS86713 486055E12	BE475748 946048C03	AW330561 707029A05		BI180003 EST520948	BE345464 946035B01	BE417348 MUG020.Al	AI065720 aq92b08.x	BE416603 MUG009.D0	BI922800 EST542704
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS	ORGANISM

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                                                                                                                                                                                                                                                  Score 358; DB 10; Length 558;
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Contact: Cathy Ronning
The Institute for Genomic Research
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wa.v.v.a. 1707-Mixed adult tissues from Walbot lab (SK) Zea AM33055. AM33050. Mixed adult tissues from Walbot lab (SK) Zea AM33050.
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Segmandophyta, Magnoliophyta, Liliopsida; Poales; Poaces; PACC
clade; Panicoidese; Adropogenese; Zea.
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Contact: Walbot V
Department of Biological Sciences
Stanford University
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Fax: 650 723 2277
Email: walbotéstanford.edu
Plate: 946048 row: C column
Location/Qualifiers
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KEYWORDS SOURCE ORGANISM

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Contect: Cathy Romain, Fabrica (1988). The Institute for General Research 2432 ttataattoatoogactoaagoaagggtootoactatoogggagaacgoaaggtacagg 2491 2492 getteccegattactacegattgtttggecegateaaggagaagtacatteaagtegga 2551 613 TTATAATTCATCCACTCAAGCGAGGGCCTCACTATCCGGGAGAACGCAAGGTTACAGG 554 553 GCTTCCCTGATTACTACCGATTGTTTGGCCCCGATCAAGAGGAGAAGTACATTCAAGTCGGGA 494 373 GACGAACTGCGGGCGAGGCGAGGCCTCTCCTGTTGGCACCCCAGCAGGGAGGTAGTTG 314 Gaps Libraries .. 10.8%; Score 295.4; DB 9; Length 613; 98.0%; Pred. No. 3e-46; For clone info: please contact Research Genetics, I Division tel 1-800-711-6195, email cdna@resqen.com 6; Indels /clone_lib="cGTD"
/tissue_type="dormant tuber"
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TITLE JOURNAL REFERENCE AUTHORS

918315464 September 2000 918315464 September 2000 918315464 September 2000 9183154644 September 2000 918315464 September 2000 918315464 September 2000 918315464 September 2000 9183154 September 2000 918 /mode="Organ: tassels; Vector: HybrizAP; Site_1: EcoRI; Site_2: Xho; George Chuck dissected immature tassels Accentage and Jam. Sharon Stanfeld prepared the CD/NA. Library in HybrizAP. Sample insert size range was 350 bp Elkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Palcoddeac; Andropogomeae; Tea.

1. (bases 1 to 572) /ilssue_type-'tassels'
//ilssue_type-'tassels'
//dev_stage-'just after the transition from vegetative to
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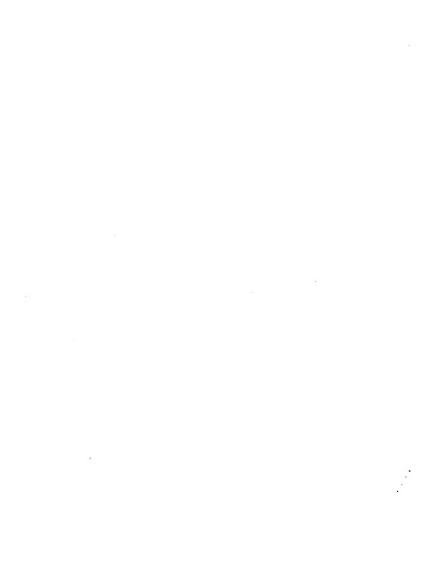
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VORDINGESTREES

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2 (bases 1 to 2232) Hearkoff, S. and Comai,L. Direct Submission Submitted (19-DEC-1997) HH

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/product-"chromomethylase" /protein_id-"AAB95486.1" /db_xref="G1:2766715" /allele="Care-1" <1. .>2232 /gene="CMT1" /codon_start=1

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Enkayord, Wirdiglances, Streptophyta; Embryophyta; Trachmophyta,
Spenatophyta; Magnollophyta, Lillopsida; Poaless; Poacess;
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57672 TPTGGTGTGTGCAATTTTGAAGECEAAATKTGTAAKTGGAAACGTCGTGAAA 57613
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Standard 14-cor-2010 Department of Plant Genetics & Breeding,
Shahtreed 14-cor-2010 Department of Plant Genetics & Breeding,
China Agricultural University, Bedjing, Bedjing 100094, China
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1 89721: contig of 85721 bp in length.
Location/Qualifiers
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Matches 246; Conservative 0; Mismatches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 112605 AAATTTGCAGATGGATTCCTTGGACGCTATGCAATGCATTGCCTTGTGGCTATGAATTAT 112546
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		REFERENCE AUTHORS	Rosidae; aurosida II, Brassicales; Brassicacese; Arabidopsis. Il (bases 1928 to 11359) Rueller, M. R., Muendlein, A., Felber, R., Mewes, H.W., Lemcke, K. and
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	DEPALERING CHARREST SPSSIFIED AND ALL	REFERENCE	4 (bases 1 to 28924) Hilbert, H., Brann, M., Holzer, E., Brandt, A., Duesterhoeft, A.,
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dene	/number=2 1754320028		lemcke@mips.blochem.mpg.de.mayer@mips.blochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
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gb!AAF20996.1|AF208044_1 [Arabidopsis thallans]"
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Substituted (19.4A-2001) The Institute for Genomic Research, 9712

Heddool Center Dr. Rockville, MC 20850, USA, edtownetigr.org

Modical Center Dr. Rockville, MC 20850, USA, edtownetigr.org

Modicas all correspondence Version replaced gl:12280892.

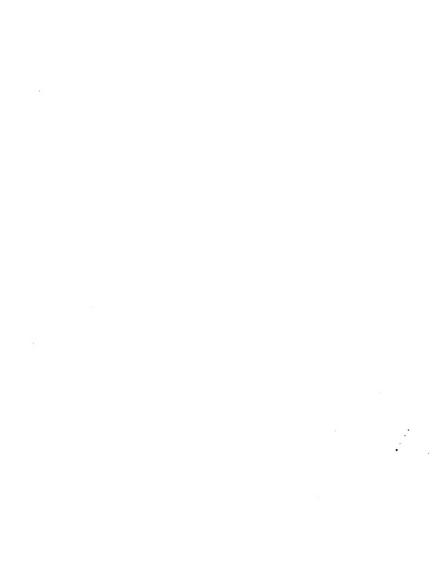
Address all correspondence to:aftligr.org
                                                                                                                                                                                                                                                                                                              Submitted (06-NOV-1999) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, ND 20850, USA, xiln@tigr.org 3 (bases 1 to 87148) Tryon.C.D. and Kauli.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC clone T6C23 is from Arabidopsis thallana chromosome 1
The orientation of the Sequence is from SP6 to T7 end of the BAC
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/dp.ctein_id="Ax55256.1"
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                                                   Maize; corn; zmet2a; DNA methyltransferase; cytosine-5-methyltransferase; DNA methylation; marker-alded selection; rhromosome segregation; DNA fingerpritting; gene therapy; trinucleotide repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel zmet2a and zmet2b methyltransferase nucleic acid sequences of Sea mays used for stabilizing transpers expression. Altering yleth or blochemical qualities, and silecting targeted genes in transgenic
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/note="this sequence contains an in-frame stop codon represented by Xaa in the protein sequence"
/partial
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Zea mays zmet2a methyltransferase coding sequence #2.
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1larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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/product= "zmet2a #2"
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(PION-) PIONEER HI-BRED INT I
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Best Local Similarity
Matches 2736; Conserv
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09-DEC-1999;
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The present sequence is one version of the oddin sequence for the maize optobler-semblitzenstease mently. The oddin sequence for the maize optobler-semblitzenstease mently. The protein encoded by this sequence is a monoval in the mently allocation of the MAN in severals for tormal anticless sequence can be used in the production of thomsent points anticless sequences can be used in the production of thomsent points with street students are settly after in one settlering, in the street of the mently and the production of the option of the opti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2419 cetcacaaccaggttataattcatccgactcaagcaagggtectcactatccgggagaac 2478
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                                                                                Novel zmet2a and zmet2b methyltransferase uncleic acid sequences of 
mays used for stabilizing transpere expression, altering Yield or 
blochemical qualities, and silencing targeted genes in transpenic
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Pred. No. 2.2e-135;
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          2000-587430755
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     WPI; 2000-587430/
P-PSDB; AAB26244.
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/note= 'this sequence contains an in-frame stop codons
given as Xaa in the protein sequence"
/patial
ccgatcaaggagaagtacattcaagtcgggaacgcagtggctgtccctgttgcccgggca 2610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctcactatccgggagaaagcaaggttacagggcttccccgattactaccgattgtttggc 2520
                                                                                                                                                                                                                                                                                                                                                     otcactatccgggagaacgcaaggttacagggcttccccgattactaccgattgtttggc 2550
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(PION-) PIONEER HI-BRED INT INC.
(MINU ) UNIV MINNESOTA.
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DD 701 HOLLING - 1999/990-000-0991-0-099-098-09-09-09-09-09-09-09-09-09-09-09-09-09-	AMASS22 standard, DNA, 12810 RP. DAMASS22 standard, DNA, 12810 RP. CAMASS22) RC AMASS220; RC AMASS20 RPHIP-1 (Usion construct.	FOR MALLE, COTT, EMELTA: DAN methyltransferase; cytosine-5-methyltransferase; MR DAN methyltransferase; MR DAN methyltransferase; MR DAN methyltransferase; MR DAN METHORITY CONTRACT, CATAGORY CATAGORY CONTRACT, CATAGORY CONTRACT, CATAGORY CONTRACT, CATAGORY CATAG	Primer_bind (1971) Primer_bind (1971)		primer_bind complement (1895-1819) Primer_bind complement (1895-1818) Primer_bind complement (1805-1818) Primer_bind (1805-1818) Primer_bind (1805-1818) Primer_bind (1805-1818) Primer_bind (1805-1818) Primer_bind complement (1806-1818) Primer_bind complement (1806-1818) Primer_bind (1806-1818)	

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                                                                                                                                                                                                                                                                                                                                  Reverse genetic strategy; Targeted Induced Local Lesions in Genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying functional mutations in genes, useful e.g. for gene function or interaction studies in plants. by mutagenests, emplification and formation of mismatched heteroduplaxes
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27,.502
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                                                                   AAS15381 standard: DNA: 520 BP
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                                                                                                                                                                                                                                                               Novel zmet2a and zmet2b methyltransferase nucleic acid sequences of Zea mays used for stablilising transpene expression, altering yield or blochemical qualities, and silencing targeted genes in transcenic
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Pred. No. 9.6e-100;
0; Mismatches 7; Indels 1; G
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(WISC ) WISCONSIN ALUMNI RES FOUND. (PION-) PIONEER HI-BRED INT INC.
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Best Local Similarity 98.4%;
Matches 482; Conservative C
                                                                                                                               Springer NM.
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                                                                                                       New fusion proteins resistant to proteolytic degradation -
comprising a core protein with a stabilishing polypeptide comprising
a peptide sequence containing blycine repeats
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48.4%; Pred. No. 8.8e-10;
tlive 0; Mismatches 278;
                                                                                                                                                                                                                                                                                                    Disclosure; Fig 3; 120pp; English
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                  P-PSDB; AAW79128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caagegegettggaatgatggtggtggttgctatggtctgccacagttcaggatgcgt 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1516 ggtgatgttgatgtcatttgtggaggcccaccatgccaaggtatcagtgqqtttaatcgg 1575
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The present DNA sequence encodes for Arabidopsis thaliana CWT3 (chromoethylase 3), a DNA methyltransferase homologue with a chromodomain.
                                                                                                                                                                                                                                                                                                                                                   Score 154.4: DR 22: Length 520:
                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.3e-26;
0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a //product= "stabilising polypeptide""
                                                                                                                                                                                                      Sequence 520 BP; 132 A; 82 C; 127 G; 179 T; 0 other;
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Stably transfecting eukaryotic cells with at least one episome for the production of a desired protein in vitro and for gene therapy -
                                                                  ccggggaaggaagaagggggatgccgagatgaaggagcccgtggaggacgacgtgtgc 249
                                                                                                                                     310 atgcaggaggaggtggttgcgggtcgcgggggtcacccgggaagaagagggggggaga 369
                                                                                                                                                                                                                                                                                                                                                                                                                      430 geggaegaggaggaggaactggcccaagcgctacggccgcagcactgccgcaaagaa 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 ccggatgaggaggaagagctcaaggccagatgtcactaccggagcgctaaggtggacaac 549
678 дадсаддаддадсаддадс---аддаддаддаддадсаддадсаддадсаддадсаддад
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BBV; nuclear antigen 1; EBNAl; episome; transfection; selection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA50254 standard: DNA: 1926 BP
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comprising a core protein with a stabilishing polypeptide comprising
comprise sequence confaining glytine repeats
                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of the stabilising sequence-encoding insert.
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48.5%; Pred. No. 2.6e-09;
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0; Mismatches 268;
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                                                                                                                                     AAV55831 standard; DNA; 799 BP.
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96US-0030986.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Epstein-barr virus,
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Sequence 1926 BP; 487 A; 352 C; 872 G; 215 T; 0 other;

selection factors, such as antibiotics.

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Query Match 2.9%; Score 78.6; DB 21; Length 1926; BB 28st Local Similarity 48.5%; Pared. No. 1.5-08; Matches 215; Conservative 0; Mismatches 239; Indels 0;
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EBV tethering protein EBNAl encoding DNA.

29-JUN-2001 AAF82902:

AAF82902 standard; DNA; 1926 (first entry)

AAF82902

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The invention provides a composition constitution by protein and expression vector operationally emcoding a protein satisfact the reduction for motification of profession where the recentled houself the foreign the reduction of profession where the recentled of the viral bink in the best cell. The viral vector second process satisfact for technique plan to introduce in recently viral procession and the reduction of the viral vector account of the viral procession and the reduction of the viral constitution of developing by meaning of that transfer to procession satisfactions of developing by meaning of that transfer to procession and the reduction of the procession and the viral transfer to procession and the viral transfer to procession and the viral transfer to procession that the viral transfer to procession the viral transfer of antitype adjacent on a sequence of the patient beart virus (RM) technicips processing by medicatida sequence of the Patient beart virus
Histone Hi; tethering protein; LANA; gene therapy, multiple sclerosis; 
Parkinson's disease; Huntington disease; diabecs; human herpeavirus 6; 
EBV; lateney-sasociated nuclear antigen; LANA; EBNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition for use in gene therapy comprises an expression vector hat includes a nucleic acid sequence encoding a nucleic acid binding
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2.9%; Score 78.6; DB 22;
Best Local Similarity 48.7%; Pred: NO. 1.5e-08;
Best Focal Similarity 48.7%; Pred: NO. 1.5e-08;
Best Focal Similarity 48.7%;
Best Local Similarity 48.7%;
Best Local Similarity 48.7%;
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                                                                                                                                                                                                                                                                                         29-SEP-2000; 2000MO-USZ6908.
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                                                                                      Spatein-barr virus.
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/product= "EBNA 1 protein"
/note= "Epstein Barr Virus Nuclear Antigen 1"
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complement (3032..4957)
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430 goggacgaggogogogoagoaactggcocaagogotacggcogcagcactgccgcaaagaaa 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Origin of replication; protein-protein interaction; replication;
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Pred. No. 1.6e-08;
0; Mismatches 229; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of the Eostein Barr nuclear antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              two-hybrid system; nuclear antigen; ss.
                                                                                                                                                                                                                                                                                                                                                                        490 ccggatgaggaggagctcaagg 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA75454 standard; DNA; 2580 BP
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This investign describes a novel method for questrating an antistance of critical investignment of a selected MN transcript. The methods on be used for identifying antisement system and for identifying antisement system and for identifying system and the state of maintainess mediated inhibition of a salected speed in the use of a direct in the state of a salected speed in the use of a salected speed in the use of a direct in this sequence in the system and in the speed at the value of a first sequence of the system of the system
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                                                                                                                                                                                                                                                                                                        Production of antisense libraries, used for identifying antisense agents and for identifying target sites for antisense-mediated inhibition of a selected gene
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Pred. No. 2.6e-08;
0; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Page 43-50; 63pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gabs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5452;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5452 BP; 1108 A; 1736 C; 1246 G; 1362 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78.6; DB 20;
Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0: Mismatches 229:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1502 GGCCAGGAGGGCCAGGAGCAGGAGG 1478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.9%;
Best Local Similarity 48.5%;
Matches 216; Conservative
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G_i protein coupled receptor; G_IPCR; G_la protein; cytoplasmic calcium; coloium mobilization; noticeptin receptor; nebmodic receptor; CRR31, neteleuxin 8 receptor type 8; episomal expression vector; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   989 ჟიცვიცემიი გამემი გამიმი გამიმი გამიმი გამიმი გ
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                                                                                                                                                                                                                                                                                        70 gaggagatccaccagaacaaggaggaggaggaggtcgcggcgtcctccgccaag 129
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                    ..
                                                                                                                                               Length 9600;
                                     Sequence 9600 BP; 2326 A; 2376 C; 2817 G; 2081 T; 0 other;
                                                                                                                                                                                                                    Indels
                                                                                                                                        Score 78.6; DB 19;
Pred. No. 2.7e-08;
0; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of pCEP4 vector.
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                                                                                                                                               Natch 2.9%;
Local Similarity 48.5%;
les 216; Conservative
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                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag" e
//otce="CMV immediate-early enhancer/promoter"
6818..7050
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/note= "bovine growth hormone polyA seguence"
                                                                           Polynucleotide delivery; plasmid pCMVKmITR-EPI; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dubois-Stringfellow N, Dwarki V, Innis MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_type INVERTED
/note= "AAV inverted terminal repeat"
7189.7355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "AAV inverted terminal repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag- b
/note= "EBV origin of replication"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "EBV nuclear antigen A"
                                                                                                          gene therapy; vaccine; polycationic agent; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_type= INVERTED
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
14..2594
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                                                                                                                                                                              Chimeric - Epstein-Barr virus.
Chimeric - Adeno-associated virus.
Chimeric - Cytomegalovirus.
Chimeric - Bos taurus.
Vector plasmid pCMVKmITR-EPI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
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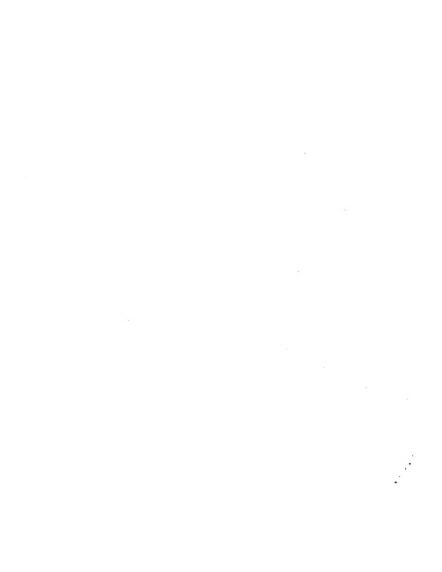
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Pipsani pCistorio (i page destruttue) is an espisania Cuy dirtuen
operassion plasmid, Heidfe variants with enhanced receptor binding
eactivity west produced by Steid-directed missensais Stable
populations of preferred MGF variants were obtained by transfecting
human embryonic kidney 33 calls and then these were succioned in
pcissons, See AARS304-55394 for examples of pref. MGF variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatocyte growth factor variants - are resistant to proteolytic 
cleavage into its two-chain form, used to treat malignancies
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7/note- "Tr5 neomycin phosphotransferase gene"
7/note- "Tr5 neomycin phosphotransferase gene"
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"CMV enhancer/promoter"
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/note= "family of repeats"
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/label~ EBNA-1
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                                                         The provision relates to ecult tronsferred with a good encoding a 6_2 protein compiled respon (G_REN) and with a game coding for a 6_1 a protein compiled receiping to the G_REN, to increase the dryologisation and the protein comparing the factor of G_REN, the massive the dryologisation and the state or executed for the difference of G_REN. The matched can cell an easy a test or executed for the difference of G_REN. The matched can cell associated which strategic limits relation and limit the difference of G_REN, the matched can cell associated the difference of G_REN, the matched can cell associated the difference of G_REN, the matched can cell associated the difference of G_REN, the matched the difference of G_REN, the difference of G_
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Pred. No. 2.76-08;
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Best Local Similarity 48.5
Matches 216; Conservative
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SQ Sequence 10596 BP; 2625 A; 2571 C; 3024 G; 2376 T; 0 other;
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Page 1

65 2.4 2301 1 US-08-306-6918-23 Sequence 23, 65 2.4 2301 5 PCT-1893-06251-78 Sequence 78, 61.4 2.2 1505 1 US-07-915-246-1 Sequence 1,	61.2 2.2 8438 1 US-07-942-283-1 Sequence 1, 60.8 2.2 390 4 US-09-197-649-7 Sequence 36, 59.6 2.2 1864 1 US-08-454-720A-38 Sequence 36,	34 95.2 2.2 1748 3 185-04.20(730-7) Sequence 1, Appl. 35 41.6 2.0 2.27 198-08.67(-9)7-2 Sequence 2, Appl. 35 41.6 2.0 2.277 198-08.67(-9)7-2 Sequence 2, Appl. 37 41.6 2.0 2.277 1 198-08.67(-9)7-2 Sequence 2, Appl. 31.6 2.0 2.277 1 198-08.67(-9)7-2 Sequence 2, Appl. 31.6 2.0 2.277 1 198-09.67(-9)7-2 Sequence 2, Appl. 31.6 2.0 2.277 1 198-09.67(-9)7-2 Sequence 2, Appl. 31.6 2.0 2.277 1 198-09.77(-9)7-2 Sequence 2, Appl. 31.6 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	29 54.14 2.0 53773 3 05.06583126-1 55400000000000000000000000000000000000	53.4 2.0 3747 4 US-05-05-05-05-1 Sequence 53.4 2.0 15378 3 US-05-35-1 Sequence 53.4 2.0 15378 3 US-05-35-1 Sequence 53.1 2.0 15378 3 US-05-35-31 Sequence	77 manuantage T_coc_oot=_oo_eo 7 Tc/T 6:T 7:cc	ALIGNMENTS	RESULT 1	Separation 18, Application US/09130114 Separation 2, Application US/09130114 Separation 2, September 18, Application US/09130114 Separation 18, US/09130114	A PRICOMPT DESIGN TARREST TO THE OFFICE ALS SCADIA PROPERTIES TO THE OFFICE TO THE OFF	OWERANCE : BALL ID NOST 39 OF Windows Version 3.0 SOFTWINE: Residue: Residu	1 1785 WAR 1 OKGATE WAR 1 US-09-130-114-2		Query:Ma Best Loc Matches	Qy 44 crigatosgasagosgascosgasgagosgasgagascosgasgagagagagagg 1	Oy 104 agglogogogogococcogocaagogogocaagogogoatctcocggaaqaago 163 by 034 avgrocyavcaacaacaacaacaacaacaacaacaacaacaacaaca		B64 AGACGGGAGGACGGGAGGAGGACGACGACGAGGACGGGGAGGA	Oy 224 agrandecettyagagedsagtyagetyagetyagagagagagagagagagagagagaggg 283 C	284 gcgaggaggacgaggagcaggcatgcaggaggaggtggttgcggtcgcgggggtt	744 AGGACGAGGACGGGGAGGACGACGAGGACGGGGAGGACGAGGGCGAGGACGAGGACGGG	DD 684 AGGACGGGGAAGGACGAGGACGAGGGGGAGGACGAGGACGGGCACGCGGGGGG	
GenCore version 4.5 COPFILGht (c) 1993 - 2000 Compagn Ltd.	OM nucleic - nucleic search, using sw model	Run on: July 15, 2002, 09:15:38 ; Search time 79.05 Seconds (Virbout of Alignments) (SOC)	Titla: 16-09-914-001-1 Perfect sore: 2736 1 atggcgccgagctcccc9tccaggggagggagtagttgagcag 2736	Scoring table: IDEMTITY_NUC Gapop 10:0, Gapext 1.0	Searched: 383533 seqs, 122816752 residues	Total number of hits satisfying chosen parameters: 767066	Midimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match ON Maximum March No Maximum March State of Summaries Listing first 45 summaries	Issued Datesta, Mar. Issued Datesta, Issued Datesta, Mar. Iss	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is electred by analysis of the total score distribution.		Result Query No. Score Match Length DB ID Description	93.2 3.4 1931 2 US-09-130-114-2 Sequence 2, 79.4 2.9 7181 1 US-09-222-463-14 Sequence 14 78.6 2.9 2860 3 US-09-000-663-2 Sequence 2.5 Sequence 2.5 2.5 2860 3 US-09-000-663-2	4 US-09-359-081-2 Sequence 2, A US-09-130-114-1 Sequence 1, A US-09-310-614-1 Sequence 1, A US-09-910-64-1	78.6 2.9 10596 1 78.6 2.9 10596 1 78.6 2.9 10596 1	11 78.6 2.9 10596 2 05-09-194-087-15 Sequence 15, 12 78.6 2.9 10596 5 107-1059-04648-15 Sequence 15, 13 76, 2 8 41349 3 115-08-281-801-200	14 75.4 2.8 1644.2 US-08-721.20 Sequence 209, 15 70.4 2.6 3489 2 US-08-728-323A-1 Sequence 1, Mc	70.4 2.6 32207 2 US-08-707-0539-20 Sequence 20, 70.4 2.6 32207 4 US-08-757-6698-20 Sequence 20, 70.4 2.6 32207 4 US-09-220-371A-20 Sequence 20,	69.4 2.5 1548 4 US-09-702.1005 Sequence 5, 69.4 2.5 1581 2 US-08-762-106-6 Sequence 6,	69.4 2.5 1581 4 US-09-120-774-6 Sequence 5, 66.8 2.4 2277 1 US-08-676-967-5 Sequence 5,	bb.8 2.4 2277 1 US-08-b7-874-5 Sequence 5, 66.8 2.4 2277 2 US-09-08-487-5 Sequence 5, 66 2.4 1771 2 US-08-533-669A-7 Sequence 7,	66 2.4

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STREET: 4 Embarcadero Center, Suite 3400
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TELECOMMUNICATION INFORMATION:
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Patent No. 6114111
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TELEPAX: (415) 740-1899
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
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APPLICANT: Horilot, Homert A.
APPLICANT: Horilot, Homert A.
APPLICANT: Robbins, Alm X.
APPLICANT: Robbins, APPLICANT: 1991-06-06
GURBERA PRILITED ANNE: 1991-06-06
GURBERA PRILITED ANNE: 1991-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.9%; Score 78.6; DB 4; Length 25 48.5%; Pred. No. 3.7e-10; tive 0; Mismatches 229; Indels
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48.5%; Pred. No. 5.2e-10;
tive 0; Mismatches 229;
SEQUENCE CHARACTERIESTICS:
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Patent No. 5976807
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Best Local Similarity 48.5%
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                                                                                                                                                                          70 gaggagatccaccagaacaaggaggaggaggaggaggcgtcctccgccaag 129
                                          0; Gaps
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CITT: San Francisco
STATE: CA
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APPLICATION NUMBER: 09/050,863
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Patent No. 6316223
GENERAL INFORMATION:
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Payan, Don
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                                          Matches 216; Conservative
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US-09-359-081-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATE, Geoderl, Paul J. Loker, Methalie A. Mark, Malanie R. TITLE OF INVESTIGATION: STRUK-COLIN STRUKE-COLIN STRUKE-COLIN STRUKE-COLIN STRUKE-COLIN STRUKE-COLIN STRUKE-COLIN STRUKE-COLIN STRUKE-COLIN STRUKE-COLIN STR
                                           Query Match 2.9%, Score 78.6; DB 4; Length 96. Best Local Similarity 48.5%, Pred. Mo. 6.7e-10; Matches 216; Conservative () Mismatches 229; Indels Matches 216; Conservative () Mismatches 229; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/884,811
FILING DATE: 19920518
CLASSIFICATION: 530
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OPERATING SYSTEM: PC-DOS/MS-DOS
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US-07-884-811-15

Sequence 15, Application US/07884811

Patent No. 5316921

GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 755
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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190 ccggggaagaagaagaagaaggggatgccgagatgaaggagcccgtggaggacgacgtgtgc 249
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                                                                                            130 cgcagccgcaaggcggcatcttccgggaagacccaagtcgcccccaagcaggccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zuckermann et al.
TITLE OF INTENTION: Compositions and Methods for TITLE OF INVENTION: Polynucleotide Delivery NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910.647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1502 GGGCAGGAGGAGCAGGAGG 1478
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6251433
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STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fujita, Sharon M.
RECISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 121
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TELEFAN: (510) 923-2706
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
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, Molecule TYPE: DNA (genomic)
US-08-910-647-1
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 egcagoogcaaggoggcatottoogggaagaagcocaagtogcoccaagcaggcoaag
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
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CONTRESPONDED.E ADDRESSEE: ADDRESSEE: Genericch, Inc.
STREET: 460 Point San Brunc Blvd
CITY: South San Francisco
STATE: California
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; Patent No. 5547856
                                                              ATTORNEY/AGENT INFORMATION:
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        FILING DATE:
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US-07-885-971-15
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STREET OF THE SEGURES. INC.
STREET OF DEATH AND THE SEGURES. THE SEGUR
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48.5%; Pred, No. 7.1e-10;
tive 0; Mismatches 229; Indels 0;
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CHERTOR WITH PRINTS 1.5.2 HIGH. 130 Rb floopy disk benchmarkers. The prints 1.5.2 High some properties of the prints of the prints 1.5.2 High some properties of the prints of the prints 1.5 High some properties of the prints 1.5 High some properties of the prints 1.5 High some properties of the prints 1.5 High some pri
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 48.5
Matches 216; Conservative
                                                                                                                                                                                                                      STRANDEDNESS: single
; TOPOLOGY: linear
US-07-884-811-15
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190 cogggagagaagaagaagaagggatgccyagatgccyagagacccytgaagaacgacgtgtgc 249
283 AwgalogaagaagaagaagggatgccyaGaccyaGaccyaGaccyaCaccyaGaccyaGaccyaCaccyaGaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCaccyaCacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 goggacgaggcgcacagcaactggcccaagcgctacggccgcagcactgccgcaaagaaa 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 gaggagatccaccagaacaaggaggaggaggaggaggtcgcggcggcggccaag 129
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CHERTON AND ALL POPER,

CHERTON TO CHERTON AS A LOS OF THE CHERTON CHERTO
                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2883 GGCAGGAGGGCAGCAGGAGG 2907
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APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-1992
ATTORNEYAGENT INFORMATION:
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                     STATE: California
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US-08-194-088B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 gccgaggagcccgacgaggaggagttggccatgggcgaggaggaggccgaggac 309
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1 Sequence 15. Application (S/08)4088

PRIENT NOT SERVICES: Paul J. LONKEY, NEIDALE A. MARK, MEIRIDE R. FEPRINGEN, THYOSHOTON: STATE OF SERVICES SERVICES SERVICES WARRANTS
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Pred. No. 7.1e-10;
0; Mismatches 229; Indels 0;
                                                                  13-701-1993
N: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                            SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAX-92
ATTORNEY/AGENT INFORMATION:
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TELEPRAY : 4792-90-.
TELER X : 410.71-716
TELER X : 910.71-716
TELER X : 910.71-71
TELER X : 910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MAISCHANG, DIANG L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
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Best Local Similarity 48.5%;
Matches 216; Conservative
                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                              PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-087-783A-15
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Gaps ö Length 10596;

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130 egcageegcegcageatetteegggaagaageecaagtegeeceecaageageeaag 189
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430 geggaegaggegegeageaactggeceaagegetaeggeegeageaetgeegeaaagaaa 489
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2.94; Score 78.6; DB 5; Length 11
Baset Local Similarity 48.54; Pred. No. 7.1.er. 10;
Matches 216; Conservative 0; Mismatches 229; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: 5.25 inch, 360 Kb floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genentech)
CURENT APPLICATION DATA:
PILING DATE: 19930517
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                                                                                                   2883 GGCAGGAGGCCAGGAGG 2907
                                                                           490 ccqqatgaqqaqqaaqqctcaaqq 514
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APPLICATION NUMBER: 07/844811
FILING DATE: 18-WAY-92
APPLICATION NUMBER: 07/8485971
ATTORNEY, ASSET 18-WAY-92
ATTORNEY, ASSET 18-WAY-92
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REGISTRATION NUMBER: 33,055
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TELEPHONE: 415/225-3216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inc
COMPUTER: IBM PC com
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                                                                                                                                                                       RESULT 12
PCT-US93-04648-15
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       RESULT 11.
Sequence 12. Application US/08194087
Fatest No. 5879310
CHERAL PROMATORY. Poul 7 Lobber Nothelie A. Werk Nelbnie R. 17114 OP. PROMATORY. ENCOTTE CROWN PROTESSE DOMAIN VARIANTS
NAMERS OF SEQUENCES. 21
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                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/194,087
FILING DATE: 18-NAY-1992
                                                                                                                                                                                       ADDRESSEE: Genertech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: patin (Generatech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
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TELEPHONE: 415/225-3216
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SEQUENCE CHRACTERIZIUS:
LENGTH: 10596 bases
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                               STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                       94080
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Db 16382 caadeaycanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacanechacane
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                                                                                                                                                                                                                                                                                                                                                                                                                66 gyccgaggagatccaccagaacaaggaggaggaggaggaggtcgcggcggcgtcctccgc 125
                                                                                                                                                                                                                                                                                                   Length 16442;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30
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STREET: 6300 Columbia Center, 701 Fifth Avenue
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NAME: No. 6090&ZOLenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
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APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 208, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
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TELEPA: (206) 682-601
INPORMATION FOR SEQ ID NO: 208:
SEQUENCE CHRACCTER.STICS:
LENGTH: 18442 base pairs
TYPE: aucidle acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COUNTRY: USA
ZIP: 98104-7092
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Bast Local Similarity 56.0%; Pred No. 57e-09; 
Matches 144; Conservative 0; Mismatches 113; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GREEAL, INTOMETON;
INTOMETON;
INTOMETON;
REFLICANT: B., VIOG-BLI
AFFLICANT: GARLEN, JOHN D.
AFFLICANT: MAILISH, JOHN T.
AFFLICANT: MAILISH, JOHN T.
AFFLICANT: MAILISH, JOHN T.
AFFLICANT: WESHALSHEN, SERVEN, SERVEN, SELATED TO
TITLE OF IMPORTION;
WESHALD T.

THE OF IMPORTION: MESHALS
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6300 Columbia Center, 701 Fifth Avenue
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Patent No. 6090620
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ADDRESSEE: SEED and B
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Washington
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US-08-781-891-209
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                                                                                                                              106 gtcgcggcggcgtcctccgccaagcgcaaggcgcaaggcggcatcttccgggaagaagcc 165
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306 ggccatgcaggaggaggtggttgcggtcgcggggggtcacccggggaagaagaggtggg 365
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MEDITAR TERE: FLORDY disk.
COMPUTER: IN PC COMPACTION.
OPERATING SYSTEM: PC-DOS/ANS-DOS
SOSTIMMER: PREDERING RESIDE: PC-DOS/ANS-DOS
MORREMY APPLICATION DATA:
APPLICATION DATA:
TILNED DATE:
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Patent No. 548676
GERRRAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: BOHERZY, NOY A,
APPLICANT: RUSSO, James J.
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
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MOLECULE TYPE: DNA (genomic)
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Db 16142 GAAGAAGAA 16134
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US-08-728-323A-1
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US-08-728-323A-1
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